

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/383,551B

DATE: 06/08/2001

TIME: 12:20:45

Input Set : A:\Pto.amc

Output Set: N:\CRF3\06082001\I383551B.raw

P.5

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3 <110> APPLICANT: Tamatani, Takuya
4   Tezuka, Katsunari
6 <120> TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
7   ADHESION AND SIGNAL TRANSMISSION
10 <130> FILE REFERENCE: 06501-039001
12 <140> CURRENT APPLICATION NUMBER: US 09/383,551B
13 <141> CURRENT FILING DATE: 1999-08-26
15 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00837
16 <151> PRIOR FILING DATE: 1998-02-27
18 <150> PRIOR APPLICATION NUMBER: JAPAN 09-62290
19 <151> PRIOR FILING DATE: 1997-02-27
21 <150> PRIOR APPLICATION NUMBER: JAPAN 10-62217
22 <151> PRIOR FILING DATE: 1998-02-26
24 <160> NUMBER OF SEQ ID NOS: 26
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 600
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(597)
37 <400> SEQUENCE: 1
38 atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa      48
39 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
40 1          5          10          15
42 gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata      96
43 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
44          20          25          30
46 ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc      144
47 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
48          35          40          45
50 cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat      192
51 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
52          50          55          60
54 ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg      240
55 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
56 65          70          75          80
58 aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta      288
59 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
60          85          90          95
62 tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca      336
63 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
64          100          105          110
66 att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg      384
67 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
68          115          120          125

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70 cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc      432
71 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
72      130                      135                      140
74 ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt      480
75 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
76 145                      150                      155                      160
78 att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct      528
79 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
80                      165                      170                      175
82 aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct      576
83 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
84                      180                      185                      190
86 aga ctc aca gat gtg acc cta taa      600
87 Arg Leu Thr Asp Val Thr Leu
88      195
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92 <211> LENGTH: 199
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 2
97 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
98 1                      5                      10                      15
99 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
100      20                      25                      30
101 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
102      35                      40                      45
103 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
104      50                      55                      60
105 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
106 65                      70                      75                      80
107 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
108      85                      90                      95
109 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
110      100                      105                      110
111 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Tyr Leu
112      115                      120                      125
113 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
114      130                      135                      140
115 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
116 145                      150                      155                      160
117 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
118      165                      170                      175
119 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
120      180                      185                      190
121 Arg Leu Thr Asp Val Thr Leu
122      195
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 2610
126 <212> TYPE: DNA

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127 <213> ORGANISM: Homo sapiens
129 <220> FEATURE:
130 <221> NAME/KEY: CDS
131 <222> LOCATION: (26)...(622)
133 <400> SEQUENCE: 3
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135                               Met Lys Ser Gly Leu Trp Tyr Phe Phe
136                               1           5
138 ctc ttc tgc ttg cgc att aaa gtt tta aca gga gaa atc aat ggt tct      100
139 Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser
140 10           15           20           25
142 gcc aat tat gag atg ttt ata ttt cac aac gga ggt gta caa att tta      148
143 Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu
144           30           35           40
146 tgc aaa tat cct gac att gtc cag caa ttt aaa atg cag ttg ctg aaa      196
147 Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys
148           45           50           55
150 ggg ggg caa ata ctc tgc gat ctc act aag aca aaa gga agt gga aac      244
151 Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn
152           60           65           70
154 aca gtg tcc att aag agt ctg aaa ttc tgc cat tct cag tta tcc aac      292
155 Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn
156           75           80           85
158 aac agt gtc tct ttt ttt cta tac aac ttg gac cat tct cat gcc aac      340
159 Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn
160 90           95           100           105
162 tat tac ttc tgc aac cta tca att ttt gat cct cct cct ttt aaa gta      388
163 Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val
164           110           115           120
166 act ctt aca gga gga tat ttg cat att tat gaa tca caa ctt tgt tgc      436
167 Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys
168           125           130           135
170 cag ctg aag ttc tgg tta ccc ata gga tgt gca gcc ttt gtt gta gtc      484
171 Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val
172           140           145           150
174 tgc att ttg gga tgc ata ctt att tgt tgg ctt aca aaa aag aag tat      532
175 Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr
176           155           160           165
178 tca tcc agt gtg cac gac cct aac ggt gaa tac atg ttc atg aga gca      580
179 Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala
180 170           175           180           185
182 gtg aac aca gcc aaa aaa tct aga ctc aca gat gtg acc cta      622
183 Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp Val Thr Leu
184           190           195
186 taatatggaa ctctggcacc caggcatgaa gcacgttgcc cagttttcct caacttgaag      682
187 tgcaagattc tcttatttcc gggaccacgg agagtctgac ttaactacat acatcttctg      742
188 ctggtgtttt gttcaatctg gaagaatgac tgtatcagtc aatggggatt ttaacagact      802
189 gccttggtac tgccgagtcc tctcaaaaca aacaccctct tgcaaccagc tttggagaaa      862
190 gccagctcc tgtgtgctca ctgggagtgg aatccctgtc tccacatctg ctctagcag      922

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191 tgcacagcc agtaaaacaa acacatttac aagaaaaatg ttttaaagat gccaggggta 982
192 ctgaatctgc aaagcaaatg agcagccaag gaccagcatc tgtccgcatt tcactatcat 1042
193 actacctctt ctttctgtag gggtgagaat tcctctttta atcagtcagg ggagatgctt 1102
194 caaagctggr gctattttat ttctgagatg ttgatgtgaa ctgtacatta gtacatactc 1162
195 agtactctcc ttcaattgct gaaccccgat tgaccatttt accaagactt tagatgcttt 1222
196 cttgtgccct caattttctt tttaaaaata cttctacatg actgcttgac agcccaacag 1282
197 ccactctcaa tagagagcta tgtcttacat tctttctctt gctgctcaat agttttatat 1342
198 atctatgcat acatatatac acacatatgt atataaaatt cataatgaat atatttgctt 1402
199 atattctccc tacaagaata tttttgctcc agaaagacat gttcttttct caaattcagt 1462
200 taaaatgggt tactttgttc aagttagtgg taggaaacat tgcccggagt tgaaagcaaa 1522
201 tttawtttat tctctattt tctaccatta tctatgtttt catggtgcta ttaattacaa 1582
202 gtttagttct tttttagat catattaaaa ttgcaacaa aatcatctt aatgggccag 1642
203 cattctcatg gggtagagca gaattatcat ttagcctgaa agctgcagtt actataggtt 1702
204 gctgtcagac tatacccatg gtgcctctgg gcttgacagg tcaaaatggg ccccatcagc 1762
205 ctggagcagc cctccagacc tgggtggaat tccagggttg agagactccc ctgagccaga 1822
206 ggccactagg tattcttgct cccagaggct gaagtcaccc tgggaatcac agtggctctac 1882
207 ctgcattcat aattccagga tctgtgaaga gcacatatgt gtcagggcac aattccctct 1942
208 cataaaaacc acacagcctg gaaattggcc ctggcccttc aagatagcct tctttagaat 2002
209 atgatttggc tagaaagatt cttaaatatg tggaatatga ttattcttag ctggaatatt 2062
210 ttctctactt cctgtctgca tgcccaaggc ttctgaagca gccaatgtcg atgcaacaac 2122
211 atttgtaact ttaggtaaac tgggattatg ttgtagttta acattttgta actgtgtgct 2182
212 tatagtttac aagttagacc cgatatgtca ttatgcatac ttatattatc ttaagcatgt 2242
213 gtaatgctgg atgtgtacag tacagtaact aacttgtaat ttgaatctag tatggtgttc 2302
214 tgttttcagc tgaattggac aacctgactg gctttgcaca ggtgttccct gagttgtttg 2362
215 cagggtttctg tgtgtgggtt ggggtatggg gaggagaacc ttcattggtg cccacctggc 2422
216 ctggttgtcc aagctgtgcc tcgacacatc ctcaccccaa gcatgggaca cctcaagatg 2482
217 aataataatt cacaaaattt ctgtgaaatc aaatccagtt ttaagaggag ccacttatca 2542
218 aagagatttt aacagtagta agaaggcaaa gaataaacat ttgatattca gcaactgaaa 2602
219 aaaaaaaa 2610

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221 <210> SEQ ID NO: 4

222 <211> LENGTH: 2072

223 <212> TYPE: DNA

224 <213> ORGANISM: Rattus norvegicus

226 <220> FEATURE:

227 <221> NAME/KEY: CDS

228 <222> LOCATION: (35)...(634)

230 <400> SEQUENCE: 4

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231 ctggagggga agagtgcagc tgttcttggc agac atg aag ccc tac ttc tcg tgc 55
232 Met Lys Pro Tyr Phe Ser Cys
233 1 5
235 gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat 103
236 Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
237 10 15 20
239 gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag 151
240 Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
241 25 30 35
243 att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg 199
244 Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
245 40 45 50 55

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247 ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc      247
248 Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
249          60          65          70
251 gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg      295
252 Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
253          75          80          85
255 tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag      343
256 Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln
257          90          95          100
259 ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt      391
260 Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
261          105          110          115
263 caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag      439
264 Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
265 120          125          130          135
267 ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt      487
268 Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe
269          140          145          150
271 gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa      535
272 Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys
273          155          160          165
275 aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc      583
276 Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe
277          170          175          180
279 atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt atg acc      631
280 Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Met Thr
281          185          190          195
283 tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttcccct      684
284 Ser
285 200
287 gaaacttgaa tggagaaagt cttctatattt ctggaccaca gggcatctga cttgattaac      744
288 tactgatacc tccttttggk gttttgtttg tctggatcag tgactatcag tcactcggaa      804
289 ttccagcaga ctgccctggg tttgtctgagt ccttttaagg caaacccctt cttatagaag      864
290 acccggtctca tatgtattca acaaacagac ctcaactggga tacaatcccc tctttctgcg      924
291 cctgcttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttacaaaaa      984
292 tgcagggta tgaatctgta aagtacacag gcagccattg accaccgtct gtccctgttt      1044
293 ttccagattc ttttttttcc catagagatc agcattcctt ctagaatcag acagtagagg      1104
294 gagatgcttc acaacagaag ctcttatgtt tctgagatgt tgatgaattc atgctttagt      1164
295 accaccatgt tctctaacia cttctatatt ccagctgac actgcttcag ggcttagatg      1224
296 cctgcttttg ccttcaagtc tccccttaaa gatactccca caggtctact tgggtggcctg      1284
297 cagccactct gaataggaag tttggtctac aatttcccc ctctgctget caaaaaaaaaa      1344
298 aattagtaga tatgattttc ccatattctc cctgccaag taattttttc cagcaaagac      1404
299 atctaaattc agttaatatg gtttactgtg ttgatattag tggcagtaaa catttctcag      1464
300 aatcaaagc aaattaattt tgcggtggtg tttttctacc attatcttgg gtttccatgg      1524
301 tgctattact cacaagttta gctatttttt tatgcatcat attaaagttg caagcaagca      1584
302 gagcaaccct cgggttaattg gcaaacattc tcctggggta gaatgaattg tctatttagc      1644
303 ccgaaaactg cagttttctgt ggggtggtgc cagactacag ccgtgctttg ctctggcttt      1704
304 gacaggttga aatagycctc atgascstgg aacagwactc cagactgtgc tggagtccca      1764
305 aagttaggag ggccatggag cctgggacag gctgctgctt tggctcttag gatctaggaa      1824

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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DATE: 06/08/2001

TIME: 12:20:46

Input Set : A:\Pto.amc

Output Set: N:\CRF3\06082001\I383551B.raw

L:628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
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L:686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23